

Supplemental Table. Frequency SIRT1 overexpression in colorectal cancer according to each methylation marker status

Methylation marker	Total N	SIRT1+	Odds ratio (95% confidence interval)	P value
<b>CIMP marker panel</b>				
<i>CACNA1G*</i>				0.0008
(-)	358	119 (33%)	1	
(+)	112	57 (51%)	2.08 (1.35-3.20)	
<i>CDKN2A (p16)*</i>				
(-)	326	115 (35%)	1	
(+)	144	61 (42%)	1.35 (0.90-2.01)	
<i>CRABP1*</i>				
(-)	306	110 (36%)	1	
(+)	164	66 (40%)	1.20 (0.81-1.77)	
<i>IGF2*</i>				0.008
(-)	350	119 (34%)	1	
(+)	120	57 (48%)	1.76 (1.15-2.68)	
<i>MLHI*</i>				<0.0001
(-)	407	136 (33%)	1	
(+)	63	40 (63%)	3.47 (1.99-6.02)	
<i>NEUROG1*</i>				0.03
(-)	322	110 (34%)	1	
(+)	148	66 (45%)	1.55 (1.04-2.31)	
<i>RUNX3*</i>				0.006
(-)	366	125 (34%)	1	
(+)	104	51 (49%)	1.86 (1.19-2.88)	
<i>SOCS1*</i>				0.02
(-)	388	136 (35%)	1	
(+)	82	40 (49%)	1.76 (1.09-2.85)	

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Other CpG islands

<i>CHFR</i>				
(-)	267	94 (35%)	1	
(+)	202	82 (41%)	1.26 (0.86-1.83)	
<i>HIC1</i>				
(-)	206	69 (34%)	1	
(+)	263	107 (41%)	1.36 (0.93-1.99)	
<i>IGFBP3</i>				
(-)	335	126 (38%)	1	
(+)	134	50 (37%)	0.99 (0.65-1.49)	
<i>MGMT</i>				
(-)	290	112 (39%)	1	
(+)	180	64 (36%)	0.88 (0.60-1.29)	
<i>MINT1</i>				
(-)	315	112 (36%)	1	
(+)	155	64 (41%)	1.27 (0.86-1.89)	
<i>MINT31</i>				0.006
(-)	299	98 (33%)	1	
(+)	171	78 (46%)	1.72 (1.17-2.53)	
p14 ( <i>CDKN2A/ARF</i> )				0.004
(-)	371	127 (34%)	1	
(+)	98	49 (50%)	1.92 (1.22-3.01)	
<i>WRN</i>				
(-)	282	99 (35%)	1	
(+)	187	77 (41%)	1.29 (0.88-1.89)	

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Only significant p values are described.